IMPOSING LABEL PRIORS IN GLOBAL TRACTOGRAPHY CAN RESOLVE CROSSING FIBRE AMBIGUITIES

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TARGET AUDIENCE – The diffusion tractography community.

PURPOSE – Conventional tractography suffers from ambiguous local fibre configurations, due to partial voluming and the symmetry of DWI data[1,2]. It is, for example, not possible to discriminate between crossing and kissing fibre bundles (Fig. 1) or between bending and fanning configurations, a leading cause of spurious (false positive) fibre tracks. Global tractography methods can be more robust against this issue by optimizing the fibre density in the entire image[2–4]. Here, we propose to use fibre bundle labels (e.g., *green* and *orange* in Fig. 1) as an additional prior in global tractography, and hypothesize that such prior will reduce false positive fibres.

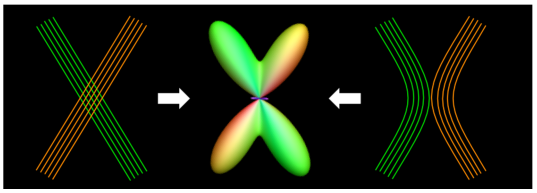

Fig. 1: Illustration of the local ambiguity in DWI data.

METHODS – *Global tractography:* Energy-based global tractography aims to reconstruct the full-brain tractogram M that best explains the data D as a whole[2–4], maximizing $P(M|D) \propto P(D|M)P(M)$. The tracks are modeled by chains of segments, that each have a fixed and equal contribution to the simulated data in the form of a fibre response function, estimated from the data[4]. The optimization, which strives for maximal similarity to the measured data subject to smoothness and connectivity priors, relies on a Markov Chain Monte Carlo technique that generates random proposals for creating, deleting, and moving segments and for (dis)connecting neighbouring segments. *Label Prior:* We introduce a white matter atlas that provides, at every position $\mathbf{x}$, the probability $p(L_\mathbf{x} = l)$ of a bundle label $L_\mathbf{x}$[5,6]. We assume that for all $\mathbf{x}$, $\sum_l p(L_\mathbf{x} = l) = 1$, and use a uniform prior in unlabelled regions. The label probability of a track t is then defined as

$$p(L_t = l) = \frac{1}{Z} \prod_{\mathbf{x} \in t} p(L_\mathbf{x} = l) \quad ,$$

where Z is the normalization across all labels l. As such, a track connecting two disjoint bundles has prior probability 0, while a track within a single bundle will have label probability 1 for that bundle. In practice, bundle label maps will overlap in crossings and due to atlas uncertainty and the attributed probabilities will not be binary. The acceptance probability (Green's ratio) of a connection proposal between tracks t_1 and t_2 is then weighted by the probability of their labels to be equal, i.e., $p(L_{t1} = L_{t2}) = \sum_l p(L_{t1} = l)p(L_{t2} = l)$. Move proposals are similarly adapted to incorporate the prior.

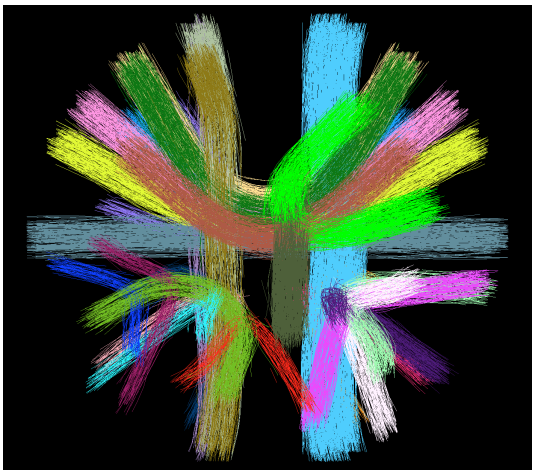

Fig. 2: Labelled track reconstruction on the Phantomas data.

Table 1: Tractometer metrics

	VC	IC	NC	VB	IB
no prior	15.9%	6.9%	77.1%	27	56
prior	19.2%	0.2%	80.6%	27	9

RESULTS – *In silico phantom:* We use the Phantomas software[7] to generate data with known ground truth fibre bundles. The data is sampled at the HCP gradient scheme (see below), at signal-to-noise ratio 30. The label probability atlas is based on the ground truth fibre bundles, using uniform probability outside white matter regions. Fig. 2 shows the reconstructed tracks, coloured by their maximum likelihood label. We compare the Tractometer metrics of this result to those without the prior in Table 1. In both cases, all 27 valid bundles (VB) are found; the number of invalid bundles (IB) is strongly reduced. With the prior, invalid connections (IC) are suppressed in favour of valid connections (VC) and at the cost of slightly increased no connections (NC). *In vivo data:* Data of a single subject is provided by the NIH Human Connectome Project, WU-Minn Consortium[8]: 18 gradients at b=0s/mm^2, 3 x 90 gradients at b=1000s/mm^2, 2000s/mm^2, and 3000s/mm^2, 1.25mm isotropic voxel size. We use the publicly available, manually segmented DTI tractography atlas of Catani and Thiebaut de Schotten[9] for creating the label probability maps (30 labels in total), normalizing all label probabilities and using a uniform prior in unlabelled regions, and register this atlas to subject-space with FSL FNIRT. The output tracks with label probability above 95% are shown in Fig. 3 for 5 bundles in the cerebrum. The forceps major substructure is segmented via an inclusion ROI in the mid-sagittal plane on reconstructions with and without label prior (Fig. 4). Imposing the prior reduces false positive fibres.

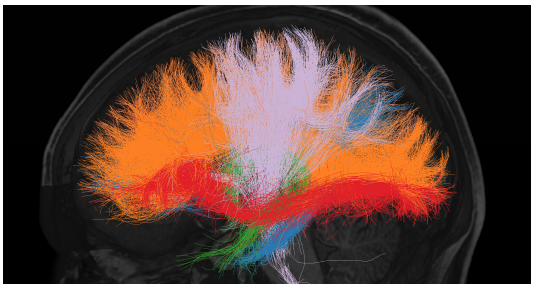

Fig. 3: Labelled tracks with probability p > 0.95: corpus callosum (*orange*), cingulum (*blue*), fornix (*green*), inferior fronto-occipital fasciculus (*red*) and corona radiata (*violet*).

DISCUSSION – The results on the in silico phantom demonstrate that imposing a "perfect" label prior effectively suppresses false positive connections. The few invalid connections that do occur either run through the grey matter area (uniform prior), or are misclassified due to edge effects at the target ROIs. In real data, bundle labelling is more difficult for two main reasons. First of all, the atlas is inherently incomplete, i.e., not all bundles are (and may never be) labelled, and some bundles are undersegmented due to the tensor-based nature of this particular atlas, e.g., the radial projections of the corpus callosum. Secondly, registration artefacts affect the labelling at the edges between neighbouring bundles, say the corpus callosum and the fornix. Nevertheless, acceptable bundle segmentations can be obtained by thresholding the label probability, and a reduction of spurious fibres demonstrates that the proposed label prior can improve the track reconstruction itself. Future work should first of all focus on building a more detailed atlas. Multi-atlas techniques may help to alleviate registration effects.

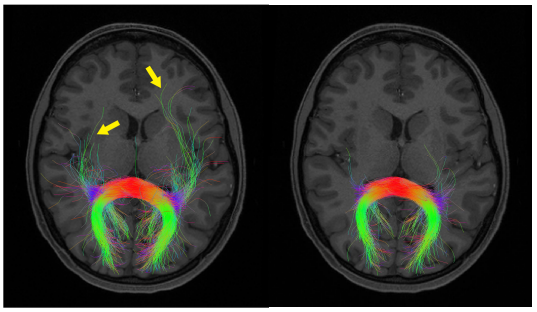

Fig. 4: Segmentation of the forceps major without label prior (*left*) and with label prior, p > 95% corpus callosum (*right*).

CONCLUSION – We have introduced a label prior in global tractography, which allows for probabilistic white matter labelling and reduces the amount of false positive fibres.

REFERENCES – 1. Jbabdi and Johansen-Berg, *Brain Connectivity 1(3):169–183* (2011); **2.** Mangin et al., *NeuroImage 80:290–296* (2013); **3.** Reisert et al., *NeuroImage 54(2):955–962* (2011); **4.** Christiaens et al., *ISMRM 22:270 (2014)*; **5.** Ziyan et al., *Int J Comput Vis 85(3):279–290* (2009); **6.** Yendiki et al., *FNINF 5(23)* (2011); **7.** Caruyer et al., *ISMRM 22:2666* (2014); **8.** Van Essen et al., *NeuroImage 80: 62–79* (2013); **9.** Catani and Thiebaut de Schotten, *Cortex 44:1105–1132* (2008).